

SEQUENCE LISTING

<110> RIKEN

<120> Sugar chain synthetase

<130> A21774A

<160> 30

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<211> 398

<212> PRT

<213> Mouse

<400> 1

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Ser Arg Leu Leu Met Glu Gly Ser Arg Glu Asp Thr Ser Gly Thr Ser

35 40 45

Ala Ala Leu Lys Thr Leu Trp Ser Pro Thr Thr Pro Val Pro Arg Thr

50 55 60

Arg Asn Ser Thr Tyr Leu Asp Glu Lys Thr Thr Gln Ile Thr Glu Lys

65 70 75 80

Cys Lys Asp Leu Gln Tyr Ser Leu Asn Ser Leu Ser Asn Lys Thr Arg

85 90 95

Arg Tyr Ser Glu Asp Asp Tyr Leu Gln Thr Ile Thr Asn Ile Gln Arg

100 105 110

Cys Pro Trp Asn Arg Gln Ala Glu Glu Tyr Asp Asn Phe Arg Ala Lys

115 120 125

Leu Ala Ser Cys Cys Asp Ala Ile Gln Asp Phe Val Val Ser Gln Asn

130 135 140

Asn Thr Pro Val Gly Thr Asn Met Ser Tyr Glu Val Glu Ser Lys Lys

145	150	155	160
His Ile Pro Ile Arg Glu Asn Ile Phe His Met Phe Pro Val Ser Gln			
165	170	175	
Pro Phe Val Asp Tyr Pro Tyr Asn Gln Cys Ala Val Val Gly Asn Gly			
180	185	190	
Gly Ile Leu Asn Lys Ser Leu Cys Gly Ala Glu Ile Asp Lys Ser Asp			
195	200	205	
Phe Val Phe Arg Cys Asn Leu Pro Pro Ile Thr Gly Ser Ala Ser Lys			
210	215	220	
Asp Val Gly Ser Lys Thr Asn Leu Val Thr Val Asn Pro Ser Ile Ile			
225	230	235	240
Thr Leu Lys Tyr Gln Asn Leu Lys Glu Lys Lys Ala Gln Phe Leu Glu			
245	250	255	
Asp Ile Ser Thr Tyr Gly Asp Ala Phe Leu Leu Leu Pro Ala Phe Ser			
260	265	270	
Tyr Arg Ala Asn Thr Gly Ile Ser Phe Lys Val Tyr Gln Thr Leu Lys			
275	280	285	
Glu Ser Lys Met Arg Gln Lys Val Leu Phe Phe His Pro Arg Tyr Leu			
290	295	300	
Arg His Leu Ala Leu Phe Trp Arg Thr Lys Gly Val Thr Ala Tyr Arg			
305	310	315	320
Leu Ser Thr Gly Leu Met Ile Ala Ser Val Ala Val Glu Leu Cys Glu			
325	330	335	
Asn Val Lys Leu Tyr Gly Phe Trp Pro Phe Ser Lys Thr Ile Glu Asp			
340	345	350	
Thr Pro Leu Ser His His Tyr Tyr Asp Asn Met Leu Pro Lys His Gly			
355	360	365	

Phe His Gln Met Pro Lys Glu Tyr Ser Gln Met Leu Gln Leu His Met

370

375

380

Arg Gly Ile Leu Lys Leu Gln Phe Ser Lys Cys Glu Thr Ala

385

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<212> DNA

<213> Mouse

<400> 2

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Met Arg Ser Gly Gly Thr Leu Phe Ala Leu Ile

1

5

10

ggc agc ctg atg ctg ctg ctc ctc ctg cgt atg ctc tgg tgc cca gcc 157

Gly Ser Leu Met Leu Leu Leu Leu Leu Arg Met Leu Trp Cys Pro Ala

15

20

25

gac gcg cct gcc cgc tcc agg ctg ttg atg gag gga agc aga gag gac 205

Asp Ala Pro Ala Arg Ser Arg Leu Leu Met Glu Gly Ser Arg Glu Asp

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35

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acc agt ggt acc tca gct gca ctg aag aca ctc tgg agc ccg aca acc 253

Thr Ser Gly Thr Ser Ala Ala Leu Lys Thr Leu Trp Ser Pro Thr Thr

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55

ccg gta cca cgc acc agg aac agc aca tat ctg gat gag aag aca acc 301

Pro Val Pro Arg Thr Arg Asn Ser Thr Tyr Leu Asp Glu Lys Thr Thr

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65

70

75

caa ata aca gag aaa tgc aaa gat ctg caa tat agc ttg aac tct tta 349

Gln Ile Thr Glu Lys Cys Lys Asp Leu Gln Tyr Ser Leu Asn Ser Leu

80

85

90

tct aac aaa acg aga cgg tac tct gag gat gac tac ctc cag acc atc	397
Ser Asn Lys Thr Arg Arg Tyr Ser Glu Asp Asp Tyr Leu Gln Thr Ile	
95 100 105	
aca aac ata cag aga tgc cca tgg aac cgg caa gca gaa gaa tat gac	445
Thr Asn Ile Gln Arg Cys Pro Trp Asn Arg Gln Ala Glu Glu Tyr Asp	
110 115 120	
aat ttt aga gca aaa ctg gct tcc tgt tgc gat gcc att caa gac ttc	493
Asn Phe Arg Ala Lys Leu Ala Ser Cys Cys Asp Ala Ile Gln Asp Phe	
125 130 135	
gtg gtt tcc cag aac aac act cca gtg ggg act aac atg agc tac gag	541
Val Val Ser Gln Asn Asn Thr Pro Val Gly Thr Asn Met Ser Tyr Glu	
140 145 150 155	
gtg gaa agc aag aaa cac atc ccc att cga gag aac att ttc cac atg	589
Val Glu Ser Lys Lys His Ile Pro Ile Arg Glu Asn Ile Phe His Met	
160 165 170	
ttt cca gtg tcg cag cct ttt gtg gac tat ccc tat aac cag tgt gca	637
Phe Pro Val Ser Gln Pro Phe Val Asp Tyr Pro Tyr Asn Gln Cys Ala	
175 180 185	
gtg gtt ggt aat ggg gga att ctc aac aag tct ctc tgc gga gca gaa	685
Val Val Gly Asn Gly Gly Ile Leu Asn Lys Ser Leu Cys Gly Ala Glu	
190 195 200	
att gat aaa tct gac ttc gtc ttc agg tgt aac ctc ccc cca atc aca	733
Ile Asp Lys Ser Asp Phe Val Phe Arg Cys Asn Leu Pro Pro Ile Thr	
205 210 215	
ggg agc gct agt aaa gat gtt gga agc aaa aca aat ctt gtg act gtc	781
Gly Ser Ala Ser Lys Asp Val Gly Ser Lys Thr Asn Leu Val Thr Val	
220 225 230 235	

aat ccc agc att ata acc ctg aag tac cag aat ttg aag gag aag aaa	829
Asn Pro Ser Ile Ile Thr Leu Lys Tyr Gln Asn Leu Lys Glu Lys Lys	
240 245 250	
gca cag ttt ttg gag gac atc tcc acc tat gga gat gca ttc ctc ctc	877
Ala Gln Phe Leu Glu Asp Ile Ser Thr Tyr Gly Asp Ala Phe Leu Leu	
255 260 265	
ctg cca gca ttt tcc tat cgg gcc aac aca ggc atc tct ttt aaa gtc	925
Leu Pro Ala Phe Ser Tyr Arg Ala Asn Thr Gly Ile Ser Phe Lys Val	
270 275 280	
tac caa aca ctc aaa gag tca aaa atg agg caa aag gtt ctc ttc ttc	973
Tyr Gln Thr Leu Lys Glu Ser Lys Met Arg Gln Lys Val Leu Phe Phe	
285 290 295	
cat ccc agg tac ctg aga cac ctc gct ctt ttc tgg aga act aaa ggg	1021
His Pro Arg Tyr Leu Arg His Leu Ala Leu Phe Trp Arg Thr Lys Gly	
300 305 310 315	
gtg act gca tac cgc ttg tcc aca ggc ttg atg att gca agt gtc gct	1069
Val Thr Ala Tyr Arg Leu Ser Thr Gly Leu Met Ile Ala Ser Val Ala	
320 325 330	
gtg gaa ctg tgt gaa aac gtg aag ctc tac gga ttc tgg cct ttc tct	1117
Val Glu Leu Cys Glu Asn Val Lys Leu Tyr Gly Phe Trp Pro Phe Ser	
335 340 345	
aag act atc gaa gac acc cca ctc agt cac cac tac tat gat aac atg	1165
Lys Thr Ile Glu Asp Thr Pro Leu Ser His His Tyr Tyr Asp Asn Met	
350 355 360	
tta cct aag cat ggt ttc cac cag atg cct aaa gaa tac agc caa atg	1213
Leu Pro Lys His Gly Phe His Gln Met Pro Lys Glu Tyr Ser Gln Met	
365 370 375	

ctc cag ctc cat atg aga gga atc ctc aaa ctg caa ttc agc aaa tgt 1261

Leu Gln Leu His Met Arg Gly Ile Leu Lys Leu Gln Phe Ser Lys Cys

370

385

390

395

gaa acg gct taa cgtttct tagaaggaga ataatttcag gaggtggagt 1310

Glu Thr Ala

398

ggatgtgtca cagcatctcc aaaaagccaa tagaagaagg cacagagaaa gcatgaatta 1370

caaaggcgct ctcccacttg tctagaccaa agccaccgcg cccactcac tttgcagcct 1430

ccacgagtca ctcatctca cttcaacgt tctttctctg agaatagaga ccaaaacatc 1490

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tgattttatt taaaatagtg aacatctact tgatatcaga cccgaggacc atcctccatt 2090

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taccacaagc atcatcatgc cagttatgaa cacagtgcctg aaaggatcat agacaggggt 2210

ggttaaactc gatcccagta gaataaactt cagtgtacct atttcagga agagttaatt 2270

tcacaattaa aactagtaaa tgaaccaatt cttaggcaca ttaagtggat tctgagtaaa 2330

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<211> 398

<212> PRT

<213> Human

<400> 3

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Ala Arg Ile Leu Val Glu Glu Ser Arg Glu Ala Thr His Gly Thr Pro

35 40 45

Ala Ala Leu Arg Thr Leu Arg Ser Pro Ala Thr Ala Val Pro Arg Ala

50 55 60

Thr Asn Ser Thr Tyr Leu Asn Glu Lys Ser Leu Gln Leu Thr Glu Lys

65 70 75 80

Cys Lys Asn Leu Gln Tyr Gly Ile Glu Ser Phe Ser Asn Lys Thr Lys

85 90 95

Gly Tyr Ser Glu Asn Asp Tyr Leu Gln Ile Ile Thr Asp Ile Gln Ser
 100 105 110
 Cys Pro Trp Lys Arg Gln Ala Glu Glu Tyr Ala Asn Phe Arg Ala Lys
 115 120 125
 Leu Ala Ser Cys Cys Asp Ala Val Gln Asn Phe Val Val Ser Gln Asn
 130 135 140
 Asn Thr Pro Val Gly Thr Asn Met Ser Tyr Glu Val Glu Ser Lys Lys
 145 150 155 160
 Glu Ile Pro Ile Lys Lys Asn Ile Phe His Met Phe Pro Val Ser Gln
 165 170 175
 Pro Phe Val Asp Tyr Pro Tyr Asn Gln Cys Ala Val Val Gly Asn Gly
 180 185 190
 Gly Ile Leu Asn Lys Ser Leu Cys Gly Thr Glu Ile Asp Lys Ser Asp
 195 200 205
 Phe Val Phe Arg Cys Asn Leu Pro Pro Thr Thr Gly Asp Val Ser Lys
 210 215 220
 Asp Val Gly Ser Lys Thr Asn Leu Val Thr Ile Asn Pro Ser Ile Ile
 225 230 235 240
 Thr Leu Lys Tyr Gly Asn Leu Lys Glu Lys Lys Ala Leu Phe Leu Glu
 245 250 255
 Asp Ile Ala Thr Tyr Gly Asp Ala Phe Phe Phe Leu Pro Ala Phe Ser
 260 265 270
 Phe Arg Ala Asn Thr Gly Thr Ser Phe Lys Val Tyr Tyr Thr Leu Glu
 275 280 285
 Glu Ser Lys Ala Arg Gln Lys Val Leu Phe Phe His Pro Lys Tyr Leu
 290 295 300
 Lys Asp Leu Ala Leu Phe Trp Arg Thr Lys Gly Val Thr Ala Tyr Arg

305 310 315 320
 Leu Ser Thr Gly Leu Met Ile Thr Ser Val Ala Val Glu Leu Cys Lys

325 330 335
 Asn Val Lys Leu Tyr Gly Phe Trp Pro Phe Ser Lys Thr Val Glu Asp

340 345 350
 Ile Pro Val Ser His His Tyr Tyr Asp Asn Lys Leu Pro Lys His Gly

355 360 365
 Phe His Gln Met Pro Lys Glu Tyr Ser Gln Ile Leu Gln Leu His Met

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 Lys Gly Ile Leu Lys Leu Gln Phe Ser Lys Cys Glu Val Ala

385 390 395

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atg cgg ccg ggg ggc gca ctg ctc gcc ctg ctc gcc agc ctg ctg ctg 139

Met Arg Pro Gly Gly Ala Leu Leu Ala Leu Leu Ala Ser Leu Leu Leu

1 5 10 15

ctg ctg ctg ctg cgc ctg ctc tgg tgc ccg gca gac gcg ccc ggc cgc 187

Leu Leu Leu Leu Arg Leu Leu Trp Cys Pro Ala Asp Ala Pro Gly Arg

20 25 30

gcc agg att ctg gtg gag gaa agc agg gag gcc acc cac ggc acc ccc 235

Ala Arg Ile Leu Val Glu Glu Ser Arg Glu Ala Thr His Gly Thr Pro

35 40 45

gca gcg ctg agg acg ctc cgg agc ccg gcg acc gcg gta ccg cgc gcc	283
Ala Ala Leu Arg Thr Leu Arg Ser Pro Ala Thr Ala Val Pro Arg Ala	
50 55 60	
act aac agc aca tat ctg aat gag aag tcg ctc caa ctg acg gag aaa	331
Thr Asn Ser Thr Tyr Leu Asn Glu Lys Ser Leu Gln Leu Thr Glu Lys	
65 70 75 80	
tgc aaa aat ctg caa tat ggc att gag tct ttc tct aac aaa acg aaa	379
Cys Lys Asn Leu Gln Tyr Gly Ile Glu Ser Phe Ser Asn Lys Thr Lys	
85 90 95	
ggg tat tca gag aac gac tac ctt cag att atc aca gat ata cag agt	427
Gly Tyr Ser Glu Asn Asp Tyr Leu Gln Ile Ile Thr Asp Ile Gln Ser	
100 105 110	
tgt cca tgg aaa cgg caa gca gaa gaa tat gca aat ttt aga gcc aaa	475
Cys Pro Trp Lys Arg Gln Ala Glu Glu Tyr Ala Asn Phe Arg Ala Lys	
115 120 125	
ctt gct tcc tgc tgt gat gct gtt caa aac ttt gtt gtt tct cag aat	523
Leu Ala Ser Cys Cys Asp Ala Val Gln Asn Phe Val Val Ser Gln Asn	
130 135 140	
aac act cca gtt ggg act aat atg agt tac gag gtg gaa agc aaa aaa	571
Asn Thr Pro Val Gly Thr Asn Met Ser Tyr Glu Val Glu Ser Lys Lys	
145 150 155 160	
gaa atc cca att aag aag aac att ttt cat atg ttt cca gtg tcc cag	619
Glu Ile Pro Ile Lys Lys Asn Ile Phe His Met Phe Pro Val Ser Gln	
165 170 175	
cct ttt gtg gac tac cct tat aat cag tgt gca gtg gtc gga aat ggg	667
Pro Phe Val Asp Tyr Pro Tyr Asn Gln Cys Ala Val Val Gly Asn Gly	
180 185 190	

gga att ctg aat aag tct ctc tgt gga act gaa ata gat aaa tcc gac	715
Gly Ile Leu Asn Lys Ser Leu Cys Gly Thr Glu Ile Asp Lys Ser Asp	
195 200 205	
ttc gtt ttt agg tgt aac cta ccc cca acc aca gga gat gtt agt aaa	763
Phe Val Phe Arg Cys Asn Leu Pro Pro Thr Thr Gly Asp Val Ser Lys	
210 215 220	
gat gtt ggc agt aaa aca aat ctt gtg act ata aat cca agc atc ata	811
Asp Val Gly Ser Lys Thr Asn Leu Val Thr Ile Asn Pro Ser Ile Ile	
225 230 235 240	
act ctg aaa tat ggg aac tta aag gaa aaa aaa gcc cta ttt ttg gag	859
Thr Leu Lys Tyr Gly Asn Leu Lys Glu Lys Lys Ala Leu Phe Leu Glu	
245 250 255	
gac att gca acc tat gga gat gca ttt ttt ttt ctg cca gca ttt tcc	907
Asp Ile Ala Thr Tyr Gly Asp Ala Phe Phe Phe Leu Pro Ala Phe Ser	
260 265 270	
ttc agg gcc aac acg ggt acc tct ttc aaa gta tac tac acg ctc gaa	955
Phe Arg Ala Asn Thr Gly Thr Ser Phe Lys Val Tyr Tyr Thr Leu Glu	
275 280 285	
gag tct aaa gca aga caa aag gtt cta ttt ttc cat ccc aag tac ctg	1003
Glu Ser Lys Ala Arg Gln Lys Val Leu Phe Phe His Pro Lys Tyr Leu	
290 295 300	
aaa gat ctg gcc ctt ttc tgg aga act aaa ggt gtg act gca tac cgc	1051
Lys Asp Leu Ala Leu Phe Trp Arg Thr Lys Gly Val Thr Ala Tyr Arg	
305 310 315 320	
ttg tcc acc ggc ttg atg atc aca agt gtt gca gtg gaa ctg tgt aaa	1099
Leu Ser Thr Gly Leu Met Ile Thr Ser Val Ala Val Glu Leu Cys Lys	
325 330 335	

aat gtg aag ctg tat gga ttc tgg ccc ttc tct aaa act gta gaa gac 1147
 Asn Val Lys Leu Tyr Gly Phe Trp Pro Phe Ser Lys Thr Val Glu Asp

340 345 350

ata cct gtc agc cat cac tat tat gac aac aag cta cct aaa cat ggt 1195
 Ile Pro Val Ser His His Tyr Tyr Asp Asn Lys Leu Pro Lys His Gly

355 360 365

ttc cat cag atg ccc aaa gaa tac agc cag atc ctc caa ctt cac atg 1243
 Phe His Gln Met Pro Lys Glu Tyr Ser Gln Ile Leu Gln Leu His Met

370 375 380

aaa gga atc ctc aaa ctg caa ttt agc aaa tgt gaa gtc gcc taa 1288
 Lys Gly Ile Leu Lys Leu Gln Phe Ser Lys Cys Glu Val Ala

385 390 395

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ccaaacacca aaggaggtgg ctaaagagta ttttgagatg agccccaaaa tttggtttga 1408

ccaaagcttc ccactcatt ttgcaatgat ggcaagtcac tcaatccttc tcattcttcat 1468

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<211> 529

<212> PRT

<213> Human

<400> 5

Met Lys Pro His Leu Lys Gln Trp Arg Gln Arg Met Leu Phe Gly Ile

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Phe Ala Trp Gly Leu Leu Phe Leu Leu Ile Phe Ile Tyr Phe Thr Asp

20 25 30

Ser Asn Pro Ala Glu Pro Val Pro Ser Ser Leu Ser Phe Leu Glu Thr

35 40 45

Arg Arg Leu Leu Pro Val Gln Gly Lys Gln Arg Ala Ile Met Gly Ala

50	55	60
Ala His Glu Pro Ser Pro Pro Gly Gly Leu Asp Ala Arg Gln Ala Leu		
65	70	75
Pro Arg Ala His Pro Ala Gly Ser Phe His Ala Gly Pro Gly Asp Leu		80
	85	90
Gln Lys Trp Ala Gln Ser Gln Asp Gly Phe Glu His Lys Glu Phe Phe		95
100	105	110
Ser Ser Gln Val Gly Arg Lys Ser Gln Ser Ala Phe Tyr Pro Glu Asp		
115	120	125
Asp Asp Tyr Phe Phe Ala Ala Gly Gln Pro Gly Trp His Ser His Thr		
130	135	140
Gln Gly Thr Leu Gly Phe Pro Ser Pro Gly Glu Pro Gly Pro Arg Glu		
145	150	155
Gly Ala Phe Pro Ala Ala Gln Val Gln Arg Arg Arg Val Lys Lys Arg		160
	165	170
His Arg Arg Gln Arg Arg Ser His Val Leu Glu Glu Gly Asp Asp Gly		175
180	185	190
Asp Arg Leu Tyr Ser Ser Met Ser Arg Ala Phe Leu Tyr Arg Leu Trp		
195	200	205
Lys Gly Asn Val Ser Ser Lys Met Leu Asn Pro Arg Leu Gln Lys Ala		
210	215	220
Met Lys Asp Tyr Leu Thr Ala Asn Lys His Gly Val Arg Phe Arg Gly		
225	230	235
Lys Arg Glu Ala Gly Leu Ser Arg Ala Gln Leu Leu Cys Gln Leu Arg		240
	245	250
Ser Arg Ala Arg Val Arg Thr Leu Asp Gly Thr Glu Ala Pro Phe Ser		255
260	265	270

Ala Leu Gly Trp Arg Arg Leu Val Pro Ala Val Pro Leu Ser Gln Leu
 275 280 285
 His Pro Arg Gly Leu Arg Ser Cys Ala Val Val Met Ser Ala Gly Ala
 290 295 300
 Ile Leu Asn Ser Ser Leu Gly Glu Glu Ile Asp Ser His Asp Ala Val
 305 310 315 320
 Leu Arg Phe Asn Ser Ala Pro Thr Arg Gly Tyr Glu Lys Asp Val Gly
 325 330 335
 Asn Lys Thr Thr Ile Arg Ile Ile Asn Ser Gln Ile Leu Thr Asn Pro
 340 345 350
 Ser His His Phe Ile Asp Ser Ser Leu Tyr Lys Asp Val Ile Leu Val
 355 360 365
 Ala Trp Asp Pro Ala Pro Tyr Ser Ala Asn Leu Asn Leu Trp Tyr Lys
 370 375 380
 Lys Pro Asp Tyr Asn Leu Phe Thr Pro Tyr Ile Gln His Arg Gln Arg
 385 390 395 400
 Asn Pro Asn Gln Pro Phe Tyr Ile Leu His Pro Lys Phe Ile Trp Gln
 405 410 415
 Leu Trp Asp Ile Ile Gln Glu Asn Thr Lys Glu Lys Ile Gln Pro Asn
 420 425 430
 Pro Pro Ser Ser Gly Phe Ile Gly Ile Leu Ile Met Met Ser Met Cys
 435 440 445
 Arg Glu Val His Val Tyr Glu Tyr Ile Pro Ser Val Arg Gln Thr Glu
 450 455 460
 Leu Cys His Tyr His Glu Leu Tyr Tyr Asp Ala Ala Cys Thr Leu Gly
 465 470 475 480
 Ala Tyr His Pro Leu Leu Tyr Glu Lys Leu Leu Val Gln Arg Leu Asn

	485	490	495
Met Gly Thr Gln Gly Asp Leu His Arg Lys Gly Lys Val Val Leu Pro			
	500	505	510
Gly Phe Gln Ala Val His Cys Pro Ala Pro Ser Pro Val Ile Pro His			
	515	520	525
Ser			
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tcattctgccacccatctgcattaagacacaaggtgctgaccgcagagacctgcc			175
atg aaa cca cac ttg aag caa tgg aga caa cga atg ctt ttc gga ata			223
Met Lys Pro His Leu Lys Gln Trp Arg Gln Arg Met Leu Phe Gly Ile			
1 5 10 15			
ttc gct tgg ggg ctc ctc ttt ttg ctg att ttc atc tac ttc acc gac			271
Phe Ala Trp Gly Leu Leu Phe Leu Leu Ile Phe Ile Tyr Phe Thr Asp			
20 25 30			
agc aac ccc gct gag cct gta ccc agc tcc ctc tcc ttc ctg gag acc			319
Ser Asn Pro Ala Glu Pro Val Pro Ser Ser Leu Ser Phe Leu Glu Thr			
35 40 45			
agg agg ctc ctg ccg gtg cag ggg aag cag cgg gcc atc atg ggc gcc			367
Arg Arg Leu Leu Pro Val Gln Gly Lys Gln Arg Ala Ile Met Gly Ala			
50 55 60			
gca cat gag ccc tcc ccg cct ggg ggc ctg gac gca cgc cag gcg ctg			415
Ala His Glu Pro Ser Pro Pro Gly Gly Leu Asp Ala Arg Gln Ala Leu			

65	70	75	80	
ccc cgc gcc cac cca gcc ggt tcc ttt cat gcg ggg cct gga gac ctg	463			
Pro Arg Ala His Pro Ala Gly Ser Phe His Ala Gly Pro Gly Asp Leu				
85	90	95		
cag aaa tgg gcc cag tcc caa gat ggg ttt gaa cat aaa gag ttt ttt	511			
Gln Lys Trp Ala Gln Ser Gln Asp Gly Phe Glu His Lys Glu Phe Phe				
100	105	110		
tca tcc cag gtg ggg aga aaa tct caa agt gct ttc tac ccg gag gat	559			
Ser Ser Gln Val Gly Arg Lys Ser Gln Ser Ala Phe Tyr Pro Glu Asp				
115	120	125		
gac gac tac ttt ttt gct gct ggt cag cca ggg tgg cac agc cac act	607			
Asp Asp Tyr Phe Phe Ala Ala Gly Gln Pro Gly Trp His Ser His Thr				
130	135	140		
cag ggg aca ttg gga ttc cct tcc ccc ggg gag cca ggc cca cgg gag	655			
Gln Gly Thr Leu Gly Phe Pro Ser Pro Gly Glu Pro Gly Pro Arg Glu				
145	150	155	160	
ggg gct ttt ccg gct gca cag gtc cag agg agg cgg gtg aag aag agg	703			
Gly Ala Phe Pro Ala Ala Gln Val Gln Arg Arg Arg Val Lys Lys Arg				
165	170	175		
cac cgg agg cag aga agg agc cac gtg ttg gag gag ggc gac gac ggc	751			
His Arg Arg Gln Arg Arg Ser His Val Leu Glu Glu Gly Asp Asp Gly				
180	185	190		
gac agg ctg tac tcc tcc atg tcc agg gcc ttc ctg tac cgg ctc tgg	799			
Asp Arg Leu Tyr Ser Ser Met Ser Arg Ala Phe Leu Tyr Arg Leu Trp				
195	200	205		
aag ggg aac gtc tct tcc aaa atg ctg aac ccg cgc ctg cag aag gcg	847			
Lys Gly Asn Val Ser Ser Lys Met Leu Asn Pro Arg Leu Gln Lys Ala				

210	215	220	
atg aag gat tac ctg acc gcc aac aag cac ggg gtg cgc ttc cgc ggg			895
Met Lys Asp Tyr Leu Thr Ala Asn Lys His Gly Val Arg Phe Arg Gly			
225	230	235	240
aag cgg gag gcc ggg ctg agc agg gca cag ctg ctg tgc cag ctg cgg			943
Lys Arg Glu Ala Gly Leu Ser Arg Ala Gln Leu Leu Cys Gln Leu Arg			
245	250	255	
agc cgc gcg cgc gtg cgg acg ctg gac gcc acc gag gcg ccc ttt tct			991
Ser Arg Ala Arg Val Arg Thr Leu Asp Gly Thr Glu Ala Pro Phe Ser			
260	265	270	
gcg ctg ggc tgg cgg cgc ctg gtg ccc gcc gtg ccc ctg agc cag ctg			1039
Ala Leu Gly Trp Arg Arg Leu Val Pro Ala Val Pro Leu Ser Gln Leu			
275	280	285	
cac ccc cgc gcc ctg cgc agc tgc gct gtc gtc atg tct gca gcc gca			1087
His Pro Arg Gly Leu Arg Ser Cys Ala Val Val Met Ser Ala Gly Ala			
290	295	300	
atc ctc aac tct tcc ttg ggc gag gaa ata gat tct cat gat gcg gtt			1135
Ile Leu Asn Ser Ser Leu Gly Glu Glu Ile Asp Ser His Asp Ala Val			
305	310	315	320
ttg aga ttt aac tct gct cct aca cgt ggt tat gag aaa gat gtt ggg			1183
Leu Arg Phe Asn Ser Ala Pro Thr Arg Gly Tyr Glu Lys Asp Val Gly			
325	330	335	
aat aaa acc acc ata cgc atc att aat tcg cag att ctg acc aac ccc			1231
Asn Lys Thr Thr Ile Arg Ile Ile Asn Ser Gln Ile Leu Thr Asn Pro			
340	345	350	
agc cat cac ttc att gac agt tca ctg tat aaa gac gtc att ttg gtg			1279
Ser His His Phe Ile Asp Ser Ser Leu Tyr Lys Asp Val Ile Leu Val			

355	360	365	
gcc tgg gac cct gcc cca tat tcc gca aat ctt aac ctg tgg tac aaa 1327			
Ala Trp Asp Pro Ala Pro Tyr Ser Ala Asn Leu Asn Leu Trp Tyr Lys			
370	375	380	
aaa ccg gat tac aac ctg ttc act cca tat att cag cat cgt cag aga 1375			
Lys Pro Asp Tyr Asn Leu Phe Thr Pro Tyr Ile Gln His Arg Gln Arg			
385	390	395	400
aac cca aat cag cca ttt tac att ctt cat cct aaa ttt ata tgg cag 1423			
Asn Pro Asn Gln Pro Phe Tyr Ile Leu His Pro Lys Phe Ile Trp Gln			
405	410	415	
ctc tgg gat att atc cag gag aac act aaa gag aag att caa cca aac 1471			
Leu Trp Asp Ile Ile Gln Glu Asn Thr Lys Glu Lys Ile Gln Pro Asn			
420	425	430	
cca cca tct tct ggt ttc att gga atc ctc atc atg atg tcc atg tgc 1519			
Pro Pro Ser Ser Gly Phe Ile Gly Ile Leu Ile Met Met Ser Met Cys			
435	440	445	
aga gag gtg cac gtg tat gaa tat atc cca tcc gtg cgg cag acg gag 1567			
Arg Glu Val His Val Tyr Glu Tyr Ile Pro Ser Val Arg Gln Thr Glu			
450	455	460	
ctg tgc cac tac cac gag ctg tac tac gac gca gcc tgc acc ctc ggg 1615			
Leu Cys His Tyr His Glu Leu Tyr Tyr Asp Ala Ala Cys Thr Leu Gly			
465	470	475	480
gcg tac cac cca cta ctc tat gag aag ctc ctg gtg cag cgc ctg aac 1663			
Ala Tyr His Pro Leu Leu Tyr Glu Lys Leu Leu Val Gln Arg Leu Asn			
485	490	495	
atg ggc acg cag ggg gat ttg cat cgc aag ggc aag gtg gtt ctt cct 1711			
Met Gly Thr Gln Gly Asp Leu His Arg Lys Gly Lys Val Val Leu Pro			

500	505	510	
ggc ttc cag gcg gtg cac tgc cct gca cca agt cca gtc att cca cac 1759			
Gly Phe Gln Ala Val His Cys Pro Ala Pro Ser Pro Val Ile Pro His			
515	520	525	
tct taaaaagggtttcttggaatcaatgtgcaatgtaca			
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Ser			
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<213> Mouse			
<400> 7			
Met Lys Pro His Leu Lys Gln Trp Arg Gln Arg Met Leu Phe Gly Ile			
1	5	10	15
Phe Val Trp Gly Leu Leu Phe Leu Ala Ile Phe Ile Tyr Phe Thr Asn			
20	25	30	
Ser Asn Pro Ala Ala Pro Met Pro Ser Ser Phe Ser Phe Leu Glu Ser			
35	40	45	
Arg Gly Leu Leu Pro Leu Gln Gly Lys Gln Arg Val Ile Met Gly Ala			
50	55	60	
Leu Gln Glu Pro Ser Leu Pro Arg Ser Leu Asp Ala Ser Lys Val Leu			
65	70	75	80
Leu Asp Ser His Pro Glu Asn Pro Phe His Pro Trp Pro Gly Asp Pro			
85	90	95	
Gln Lys Trp Asp Gln Ala Pro Asn Gly Phe Asp Asn Gly Asp Glu Phe			
100	105	110	
Phe Thr Ser Gln Val Gly Arg Lys Ser Gln Ser Ala Phe Tyr Pro Glu			
115	120	125	
Glu Asp Ser Tyr Phe Phe Val Ala Asp Gln Pro Glu Leu Tyr His His			

130	135	140
Arg Gln Gly Ala Leu Glu Leu Pro Ser Pro Gly Glu Thr Ser Trp Arg		
145	150	155
Ser Gly Pro Val Gln Pro Lys Gln Lys Leu Leu His Pro Arg Arg Gly		160
	165	170
		175
Ser Leu Pro Glu Glu Ala Tyr Asp Ser Asp Met Leu Ser Ala Ser Met		
	180	185
		190
Ser Arg Ala Phe Leu Tyr Arg Leu Trp Lys Gly Ala Val Ser Ser Lys		
	195	200
		205
Met Leu Asn Pro Arg Leu Gln Lys Ala Met Arg Tyr Tyr Met Ser Phe		
	210	215
		220
Asn Lys His Gly Val Arg Phe Arg Arg Arg Gly Arg Arg Glu Ala Thr		
225	230	235
		240
Arg Thr Gly Pro Glu Leu Leu Cys Glu Met Arg Arg Arg Val Arg Val		
	245	250
		255
Arg Thr Leu Asp Gly Arg Glu Ala Pro Phe Ser Gly Leu Gly Trp Arg		
	260	265
		270
Pro Leu Val Pro Gly Val Pro Leu Ser Gln Leu His Pro Arg Gly Leu		
	275	280
		285
Ser Ser Cys Ala Val Val Met Ser Ala Gly Ala Ile Leu Asn Ser Ser		
	290	295
		300
Leu Gly Glu Glu Ile Asp Ser His Asp Ala Val Leu Arg Phe Asn Ser		
305	310	315
		320
Ala Pro Thr Arg Gly Tyr Glu Lys Asp Val Gly Asn Lys Thr Thr Val		
	325	330
		335
Arg Ile Ile Asn Ser Gln Ile Leu Ala Asn Pro Ser His His Phe Ile		
	340	345
		350

Asp Ser Ala Leu Tyr Lys Asp Val Ile Leu Val Ala Trp Asp Pro Ala			
355	360	365	
Pro Tyr Ser Ala Asn Leu Asn Leu Trp Tyr Lys Lys Pro Asp Tyr Asn			
370	375	380	
Leu Phe Thr Pro Tyr Ile Gln His Arg Arg Lys Tyr Pro Thr Gln Pro			
385	390	395	400
Phe Tyr Ile Leu His Pro Lys Phe Ile Trp Gln Leu Trp Asp Ile Ile			
405	410	415	
Gln Glu Asn Thr Arg Glu Lys Ile Gln Pro Asn Pro Pro Ser Ser Gly			
420	425	430	
Phe Ile Gly Ile Leu Ile Met Met Ser Met Cys Lys Glu Val His Val			
435	440	445	
Tyr Glu Tyr Ile Pro Ser Val Arg Gln Thr Glu Leu Cys His Tyr His			
450	455	460	
Glu Leu Tyr Tyr Asp Ala Ala Cys Thr Leu Gly Ala Tyr His Pro Leu			
465	470	475	480
Leu Tyr Glu Lys Leu Leu Val Gln Arg Leu Asn Thr Gly Thr Gln Ala			
485	490	495	
Asp Leu His His Lys Gly Lys Val Val Leu Pro Gly Phe Gln Thr Leu			
500	505	510	
Arg Cys Pro Val Thr Ser Pro Asn Asn Thr His Ser			
515	520		

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ca atg aaa cca cac ttg aag caa tgg cga caa cga atg ctc ttt gga ata 50
 Met Lys Pro His Leu Lys Gln Trp Arg Gln Arg Met Leu Phe Gly Ile
 1 5 10 15
 ttt gtt tgg ggg ctc ctc ttt ttg gca att ttc atc tac ttc acc aac 98
 Phe Val Trp Gly Leu Leu Phe Leu Ala Ile Phe Ile Tyr Phe Thr Asn
 20 25 30
 agc aat cct gcg gca cct atg ccc agc tcc ttt tcc ttc ctg gag agc 146
 Ser Asn Pro Ala Ala Pro Met Pro Ser Ser Phe Ser Phe Leu Glu Ser
 35 40 45
 cgt ggg ctc ctg cct cta cag ggc aag cag cgg gtc atc atg ggc gct 194
 Arg Gly Leu Leu Pro Leu Gln Gly Lys Gln Arg Val Ile Met Gly Ala
 50 55 60
 ttg cag gaa ccc tct ttg ccc aga agt ttg gat gca agc aaa gtg ctt 242
 Leu Gln Glu Pro Ser Leu Pro Arg Ser Leu Asp Ala Ser Lys Val Leu
 65 70 75 80
 ctg gac agc cac cct gag aac cct ttc cac cct tgg cct ggg gac cca 290
 Leu Asp Ser His Pro Glu Asn Pro Phe His Pro Trp Pro Gly Asp Pro
 85 90 95
 cag aaa tgg gat cag gcc cca aat ggc ttt gac aat ggg gat gag ttt 338
 Gln Lys Trp Asp Gln Ala Pro Asn Gly Phe Asp Asn Gly Asp Glu Phe
 100 105 110
 ttt aca tcc cag gtt ggg agg aaa tca caa agc gct ttc tat ccc gag 386
 Phe Thr Ser Gln Val Gly Arg Lys Ser Gln Ser Ala Phe Tyr Pro Glu
 115 120 125
 gaa gat agc tat ttt ttt gtt gcg gat cag cct gag ttg tac cac cac 434
 Glu Asp Ser Tyr Phe Phe Val Ala Asp Gln Pro Glu Leu Tyr His His
 130 135 140

agg cag ggt gca ctg gag ctg cca tct cca ggg gag aca tca tgg cga 482
 Arg Gln Gly Ala Leu Glu Leu Pro Ser Pro Gly Glu Thr Ser Trp Arg
 145 150 155 160
 tca gga cct gtt cag ccc aag cag aag ctg ctt cac cca agg cga ggc 530
 Ser Gly Pro Val Gln Pro Lys Gln Lys Leu Leu His Pro Arg Arg Gly
 165 170 175
 agc ttg cct gag gaa gcc tat gac agc gac atg ctg tca gcc tcc atg 578
 Ser Leu Pro Glu Glu Ala Tyr Asp Ser Asp Met Leu Ser Ala Ser Met
 180 185 190
 tcg aga gcc ttc ctg tac cgg ctc tgg aag ggg gcc gtg tcc tct aag 626
 Ser Arg Ala Phe Leu Tyr Arg Leu Trp Lys Gly Ala Val Ser Ser Lys
 195 200 205
 atg ttg aac ccg cgc ctg cag aag gcc atg cgt tac tac atg tcc ttc 674
 Met Leu Asn Pro Arg Leu Gln Lys Ala Met Arg Tyr Tyr Met Ser Phe
 210 215 220
 aac aag cat ggt gtg cgc ttc cgc agg cgg ggt cgg cgt gaa gct aca 722
 Asn Lys His Gly Val Arg Phe Arg Arg Arg Gly Arg Arg Glu Ala Thr
 225 230 235 240
 cgt aca ggg ccg gag ctg ctg tgt gag atg cgc aga cgt gtg cgt gtg 770
 Arg Thr Gly Pro Glu Leu Leu Cys Glu Met Arg Arg Arg Val Arg Val
 245 250 255
 cgc acg ttg gac ggc aga gag gcg ccc ttc tcg ggg ctg ggc tgg cgg 818
 Arg Thr Leu Asp Gly Arg Glu Ala Pro Phe Ser Gly Leu Gly Trp Arg
 260 265 270
 cct ctg gta cca ggt gta cct ctg agc cag ttg cac ccg cgc ggt ctg 866
 Pro Leu Val Pro Gly Val Pro Leu Ser Gln Leu His Pro Arg Gly Leu
 275 280 285

agc agc tgc gca gtt gtc atg tct gcc ggt gcc atc ctg aac tcc tcc 914
 Ser Ser Cys Ala Val Val Met Ser Ala Gly Ala Ile Leu Asn Ser Ser
 290 295 300
 ttg ggg gag gaa atc gat tct cat gat gca gtt ttg aga ttt aac tct 962
 Leu Gly Glu Glu Ile Asp Ser His Asp Ala Val Leu Arg Phe Asn Ser
 305 310 315 320
 gcc cct acc cgt ggc tac gag aaa gat gtc gga aat aaa acc aca gta 1010
 Ala Pro Thr Arg Gly Tyr Glu Lys Asp Val Gly Asn Lys Thr Thr Val
 325 330 335
 cgc atc att aat tct cag att ctg gcc aac ccc agc cat cac ttc att 1058
 Arg Ile Ile Asn Ser Gln Ile Leu Ala Asn Pro Ser His His Phe Ile
 340 345 350
 gac agt gct tta tat aaa gat gtt atc ctg gta gcc tgg gat cct gct 1106
 Asp Ser Ala Leu Tyr Lys Asp Val Ile Leu Val Ala Trp Asp Pro Ala
 355 360 365
 cct tat tct gcc aat ctt aac ctg tgg tat aag aag cca gat tac aac 1154
 Pro Tyr Ser Ala Asn Leu Asn Leu Trp Tyr Lys Lys Pro Asp Tyr Asn
 370 375 380
 ctt ttc act cca tat atc cag cat cgc cgg aaa tac ccg act cag cca 1202
 Leu Phe Thr Pro Tyr Ile Gln His Arg Arg Lys Tyr Pro Thr Gln Pro
 385 390 395 400
 ttt tac att ctt cac ccc aag ttc ata tgg cag ctt tgg gac att atc 1250
 Phe Tyr Ile Leu His Pro Lys Phe Ile Trp Gln Leu Trp Asp Ile Ile
 405 410 415
 cag gag aat aca agg gag aag ata cag ccc aac cca cca tct tct ggt 1298
 Gln Glu Asn Thr Arg Glu Lys Ile Gln Pro Asn Pro Pro Ser Ser Gly
 420 425 430

ttt att gga atc ctc atc atg atg tcc atg tgt aaa gag gtg cac gtg 1346
 Phe Ile Gly Ile Leu Ile Met Met Ser Met Cys Lys Glu Val His Val
 435 440 445
 tat gag tac atc cca tct gtt cga cag aca gag ctt tgc cac tac cat 1394
 Tyr Glu Tyr Ile Pro Ser Val Arg Gln Thr Glu Leu Cys His Tyr His
 450 455 460
 gag ctg tac tac gac gca gcc tgc acc ttg ggg gcc tac cac cca ctg 1442
 Glu Leu Tyr Tyr Asp Ala Ala Cys Thr Leu Gly Ala Tyr His Pro Leu
 465 470 475 480
 ctc tat gaa aag cta ctg gtg cag cgc ctt aac aca ggc acc cag gca 1490
 Leu Tyr Glu Lys Leu Leu Val Gln Arg Leu Asn Thr Gly Thr Gln Ala
 485 490 495
 gac ttg cat cac aag ggc aag gta gtc ttg cca ggc ttc cag acc ctt 1538
 Asp Leu His His Lys Gly Lys Val Val Leu Pro Gly Phe Gln Thr Leu
 500 505 510
 cgg tgt cca gta acc agc ccc aac aat aca cat tct taa 1577
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 515 520
 aatggaactc ttgggaactg atgtgcaata aggt 1611

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 <212> DNA
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 <223> Description of Artificial Sequence: Synthetic DNA
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 cttttctgga gaactaaagg 20

<210> 10

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aattgcagtt tgaggattcc 20

<210> 11
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tggctcagga tgagatcggg 20

<210> 12
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<212> DNA
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<400> 12
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<210> 13
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<210> 17

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic DNA

<400> 17

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<210> 18

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<210> 19
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gacaatgggg atgagttttt tacatcccag 30

<210> 20
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<210> 23
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<210> 25
<211> 30
<212> DNA
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<210> 26
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21